

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 30, 2002, 12:23:18 : Search time 57.9734 Seconds

(without alignments)  
3273.388 Million cell updates/sec

US-10-054-680-2

Perfect score: 4797  
Sequence: 1 MAMLRLOPLTSAFLHFGVLT.....LMLXILEFTLEATCYIKGF 921

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL.21.\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_protist:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4768.5	99.4	924	4	Q96QGI homo sapien
2	4671	97.4	925	4	Q96QGI
3	4563.5	95.1	928	11	Q96QGI
4	3458.5	72.1	934	6	Q97801 macaca mula
5	3443.5	71.8	941	6	Q28662 oryctolagus
6	3437.5	71.7	941	6	Q97814 oryctolagus
7	3427.5	71.5	934	11	Q9R238
8	3425.5	71.4	934	11	Q9WU30
9	3417	71.2	957	11	Q9R239
10	3409.5	71.1	962	11	Q924Y2
11	3406	71.0	969	11	Q9WU29
12	3290.5	68.6	968	13	Q9PT19
13	3191.5	66.5	940	11	Q35157
14	3012	62.8	995	11	Q9EP08
15	2533	52.8	892	5	Q02196
16	2203.5	45.9	925	5	Q45630

17	2160.5	45.0	793	4	Q9H021
18	2156.5	45.0	602	6	Q9TV05
19	2130.5	44.4	950	5	Q24413
20	2130.5	44.4	950	5	Q9VDG5
21	2128.5	44.4	600	11	Q912J7
22	2126.5	44.3	600	11	Q9ET74
23	2119	44.2	950	5	Q18367
24	2102	43.8	583	13	Q91850
25	2096	43.7	955	5	Q94161
26	2001.5	41.7	880	5	Q21609
27	1912.5	39.9	560	13	Q91849
28	1278	26.6	254	13	Q9YH83
29	1192	24.8	807	5	Q21895
30	1105.5	23.0	263	13	Q9YCE0
31	1046.5	21.8	263	13	Q9YH84
32	1038	21.6	264	13	Q9YGE1
33	970.5	20.2	267	13	Q9YGE2
34	660	13.8	199	11	Q8R505
35	614.5	12.8	215	11	Q9Z0F8
36	599.5	12.5	263	5	Q8WPE2
37	579	12.1	539	10	Q22252
38	573	11.9	133	11	Q9QW49
39	523.5	10.9	171	11	Q8R504
40	487	10.2	158	6	Q9MY54
41	481	10.0	92	11	Q8R503
42	424	8.8	92	11	Q91206
43	329	6.9	107	6	Q97792
44	318	6.6	1130	11	Q91WB8
45	308	6.4	140	11	Q62614

## ALIGNMENTS

RESULT 1	Q96QGI	PRELIMINARY:	PRT:	924 AA.
ID	Q96QGI			
AC	Q96QGI			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Sodium/calcium exchanger SCL8A3.			
GN	SCL8A3.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RP	Bortoluzzi S.;			
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.			
RT	SEQUENCE FROM N.A.			
RT	Gabelini N.;			
RT	"Characterization of the human SCL8A3 gene for solute carrier family			
RT	8, member 3 (sodium/calcium exchanger).";			
RT	Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AJ304853; CAC40985.1;			
DR	InterPro: IPR003644; Calx_beta.			
DR	InterPro: IPR004837; Naca_Exemb.			
DR	InterPro: IPR004836; Na_Ca_Ex.			
DR	Pfam: PF03160; Calx_beta; 2.			
DR	Pfam: PF01699; Na_Ca_Ex; 1.			
DR	TIGRFAAS; TIGR00845; caca; 1.			
DR	TIGRFAAS; TIGR00845; caca; 1.			
DR	SEQUENCE 924 AA; 102694 MW; AOA5568753998A07 CRC64;			
Query Match	99.4%;	Score 4768.5;	DB 4;	Length 924;
Best Local Similarity	99.4%;	Pred. No. 0;		
Matches 918:	Conservative	1;	Mismatches	2;
			Indels	3;
			Gaps	1;
QY	1 MAMLRLOPLTSAFLHFGVLTFLNGLAERAGSGSDVPSIQNNESGSGSDCKEGVTL 60			
DB	1 MAMLRLOPLTSAFLHFGVLTFLNGLAERAGSGSDVPSIQNNESGSGSDCKEGVTL 60			

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QY 61 PIWYPPNSLGDKIAIYIVFVALIYMFGLVSIADRFMAISIEVITSQEREVITKKNPGE 120
DB 61 PIWYPPNSLGDKIAIYIVFVALIYMFGLVSIADRFMAISIEVITSQEREVITKKNPGE 120
QY 121 TSTTTIRVWNETYSNLTIALMGSSAPEILSLIEVCGHGIAGDLGPSTTVGSAARNFMT 180
DB 121 TSTTTIRVWNETYSNLTIALMGSSAPEILSLIEVCGHGIAGDLGPSTTVGSAARNFMT 180
QY 181 IIGICVYVDPGETRRIKHLRVFETIAMSIFVIMLYMLAVFSPGVVWBGSLTLTF 240
DB 181 IIGICVYVDPGETRRIKHLRVFETIAMSIFVIMLYMLAVFSPGVVWBGSLTLTF 240
QY 241 FPVCVLLAWADKRLLEFYKYMHKRYRTDKRGIIIEEGDHPKGIEMDGKMMNSHFLDGN 300
DB 241 FPVCVLLAWADKRLLEFYKYMHKRYRTDKRGIIIEEGDHPKGIEMDGKMMNSHFLDGN 300
QY 301 LVPLEGKVDSESRREMIIRIKDLKOKHPEKDOLQVEMANYALSHOOKSRAFYRIQATR 360
DB 301 LVPLEGKVDSESRREMIIRIKDLKOKHPEKDOLQVEMANYALSHOOKSRAFYRIQATR 360
QY 361 MMTGAGNIIKKHAAEQAKKASSMEVHTDEPEDFISKVFDPGCSYOCLENGCAVLLTVR 420
DB 361 MMTGAGNIIKKHAAEQAKKASSMEVHTDEPEDFISKVFDPGCSYOCLENGCAVLLTVR 420
QY 421 KGGDMSKTMVVDYKTEDGSAAGADYEETEGTVLKPGETOKEFVSAGIIDDIIFEDEHF 480
DB 421 KGGDMSKTMVVDYKTEDGSAAGADYEETEGTVLKPGETOKEFVSAGIIDDIIFEDEHF 480
QY 481 FVRLSNVRIEEOPEEGMPAIFNSLPLPRAVLASPCVAVTTLDDHAGITFEECTTIH 540
DB 481 FVRLSNVRIEEOPEEGMPAIFNSLPLPRAVLASPCVAVTTLDDHAGITFEECTTIH 540
QY 541 VSESIGVMEVKVLRITSGARGTIVPRTVEGTAKGGGEDEDTYGELEFKNDETAKTIRY 600
DB 541 VSESIGVMEVKVLRITSGARGTIVPRTVEGTAKGGGEDEDTYGELEFKNDETAKTIRY 600
QY 601 KIYDEEYERQENFEALGEPKMMERGISDV---TDRKLTMEEBEAKRIAEMKRPVLGEH 657
DB 601 KIYDEEYERQENFEALGEPKMMERGISDV---TDRKLTMEEBEAKRIAEMKRPVLGEH 657
QY 658 PKLEVIIEESYEKRTYDKLIKTNLALVYGTSHMRQEFMEATITVSAAGDEDESEER 717
DB 658 PKLEVIIEESYEKRTYDKLIKTNLALVYGTSHMRQEFMEATITVSAAGDEDESEER 717
QY 718 LPSCFDVYMHFLTVFMKVLFCVPTPEYCHGMAFVSIILIGMLTFAIIGDLSHFCCTI 777
DB 718 LPSCFDVYMHFLTVFMKVLFCVPTPEYCHGMAFVSIILIGMLTFAIIGDLSHFCCTI 777
QY 778 GLKDSYAVVFAVAGTISVPTFASKAALODVYADASIGNVTSNNAVNFILGILAMNSA 837
DB 778 GLKDSYAVVFAVAGTISVPTFASKAALODVYADASIGNVTSNNAVNFILGILAMNSA 837
QY 838 AIYMALOGGEFHSAGTLAGSVTLTEFAVCTISVILYRRRPHLGGELGPRCKLATTW 897
DB 838 AIYMALOGGEFHSAGTLAGSVTLTEFAVCTISVILYRRRPHLGGELGPRCKLATTW 897
QY 898 LFVSLMLLYTLFATLEAYCYIKGF 921
DB 898 LFVSLMLLYTLFATLEAYCYIKGF 921
QY 901 LFVSLMLLYTLFATLEAYCYIKGF 924
DB 901 LFVSLMLLYTLFATLEAYCYIKGF 924

RESULT 2
0960G2 PRELIMINARY: PRT: 925 AA.
AC 0960G2:
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Sodium/calcium exchanger SCL8A3.
GN SCL8A3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bortoluzzi S.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Gabelini N.;
RT "Characterization of the human SCL8A3 gene for solute carrier family
RT 8, member 3 (sodium/calcium exchanger).";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ304852; CAC40984.1; -.
DR InterPro: IPR003644; Calx_delta.
DR InterPro: IPR004837; NaCa_Exemb.
DR InterPro: IPR004836; NaCa_Ex.
DR Pfam: PF03160; Calx_delta.2.
DR Pfam: PF01699; NaCa_Ex; 2.
DR TIGRPFAM: TIGR00845; caca; 1.
DR SQUENCH 925 AA; 102803 MW; OCCF8DA0881C4FDA CRC64;
```

Query Match 97.4%; Score 4671; DB 4; Length 925;  
Best Local Similarity 96.9%; Pred. No. 0;  
Matches 896; Conservative 11; Mismatches 14; Indels 4; Gaps 1;

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QY 1 MAMLRLOPLTSAFLHGLVTVFLFNLGRAEAGSGDVPSTGONNESCSSGSDCKEGLVL 60
DB 1 MAMLRLOPLTSAFLHGLVTVFLFNLGRAEAGSGDVPSTGONNESCSSGSDCKEGLVL 60
QY 61 PIWYPPNSLGDKIAIYIVFVALIYMFGLVSIADRFMAISIEVITSQEREVITKKNPGE 120
DB 61 PIWYPPNSLGDKIAIYIVFVALIYMFGLVSIADRFMAISIEVITSQEREVITKKNPGE 120
QY 121 TSTTTIRVWNETYSNLTIALMGSSAPEILSLIEVCGHGIAGDLGPSTTVGSAARNFMT 180
DB 121 TSTTTIRVWNETYSNLTIALMGSSAPEILSLIEVCGHGIAGDLGPSTTVGSAARNFMT 180
QY 181 IIGICVYVDPGETRRIKHLRVFETIAMSIFVIMLYMLAVFSPGVVWBGSLTLTF 240
DB 181 IIGICVYVDPGETRRIKHLRVFETIAMSIFVIMLYMLAVFSPGVVWBGSLTLTF 240
QY 241 FPVCVLLAWADKRLLEFYKYMHKRYRTDKRGIIIEEGDHPKGIEMDGKMMNSHFLDGN 300
DB 241 FPVCVLLAWADKRLLEFYKYMHKRYRTDKRGIIIEEGDHPKGIEMDGKMMNSHFLDGN 300
QY 301 LVPLEGKVDSESRREMIIRIKDLKOKHPEKDOLQVEMANYALSHOOKSRAFYRIQATR 360
DB 301 LVPLEGKVDSESRREMIIRIKDLKOKHPEKDOLQVEMANYALSHOOKSRAFYRIQATR 360
QY 361 MMTGAGNIIKKHAAEQAKKASSMEVHTDEPEDFISKVFDPGCSYOCLENGCAVLLTVR 420
DB 361 MMTGAGNIIKKHAAEQAKKASSMEVHTDEPEDFISKVFDPGCSYOCLENGCAVLLTVR 420
QY 421 KGGDMSKTMVVDYKTEDGSAAGADYEETEGTVLKPGETOKEFVSAGIIDDIIFEDEHF 480
DB 421 KGGDMSKTMVVDYKTEDGSAAGADYEETEGTVLKPGETOKEFVSAGIIDDIIFEDEHF 480
QY 481 FVRLSNVRIEEOPEEGMPAIFNSLPLPRAVLASPCVAVTTLDDHAGITFEECTTIH 540
DB 481 FVRLSNVRIEEOPEEGMPAIFNSLPLPRAVLASPCVAVTTLDDHAGITFEECTTIH 540
QY 541 VSESIGVMEVKVLRITSGARGTIVPRTVEGTAKGGGEDEDTYGELEFKNDETAKTIRY 600
DB 541 VSESIGVMEVKVLRITSGARGTIVPRTVEGTAKGGGEDEDTYGELEFKNDETAKTIRY 600
QY 601 KIYDEEYERQENFEALGEPKMMERGISDV---TDRKLTMEEBEAKRIAEMKRPVLGEH 656
DB 601 KIYDEEYERQENFEALGEPKMMERGISDV---TDRKLTMEEBEAKRIAEMKRPVLGEH 656
QY 657 HPKLEVIIEESYEKRTYDKLIKTNLALVYGTSHMRQEFMEATITVSAAGDEDESEER 716
DB 657 HPKLEVIIEESYEKRTYDKLIKTNLALVYGTSHMRQEFMEATITVSAAGDEDESEER 716
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Qy	717	RLPSCFDYVNHLELVFPKKVYLEACAPYPRFXCHGNACFVSVLTIIIGMTALIIIGDLASHRGCT	776
Db	721	RLPSCFDYVNHLELVFPKKVYLEACAPYPRFXCHGNACFVSVLTIIIGMTALIIIGDLASHRGCT	780
Qy	777	IGLKDSTVAVFEVAFGTSVDPDTPFASKAAALQDYPADASIGNVTGSNNAVNFELIGLAMS	836
Db	781	IGLKDSTVAVFEVAFGTSVDPDTPFASKAAALQDYPADASIGNVTGSNNAVNFELIGLAMS	840
Qy	837	AAIYVALDQGEFHHASAGTLASVYTLFTITFAFVCIISVLLIKRRPHLGELGPGPKCIATT	896
Db	841	AAIYVALDQGEFHHASAGTLASVYTLFTITFAFVCIISVLLIKRRPHLGELGPGPKCIATT	900
Qy	897	WLFVSLMLLYTLFTATLEAYCYIKGF	921
Db	901	WLFVSLMLLYTLFTATLEAYCYIKGF	925

### RESULT 3

AD	OBVH38	PRELIMINARY;	PRT;	928 AA.
AC	OBVH38			
DT	01-MAR-2002 (Tremblrel, 20, Created)			
DT	01-MAR-2002 (Tremblrel, 20, Last sequence update)			
DT	01-JUN-2002 (Tremblrel, 21, Last annotation update)			
DE	Sodium/calcium exchanger.			
GN	SLC8A3.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=SKELTAL MUSCLE;			
RA	Kraev A.;			
RT	"Towards complete inventory of calcium transporters of the house			
RT	mouse.";			
RL	Submitted (NCV-2001) to the EMBL/GenBank/DBJ databases.			
RL	EMBL; AF453257; AAL3910.1; -			
DR	MGD; MGI:107976; Slc8a3.			
DR	InterPro: IPR003644; Calx_beta.			
DR	InterPro: IPR004837; NaCa_Exmemb.			
DR	InterPro: IPR004836; Na_Ca_Ex.			
DR	Pfam: PF03160; Calx_beta; 2.			
DR	Pfam: PF01699; Na_Ca_Ex; 2.			
DR	PRINTS; PRO1259; NACAECHNGR.			
DR	SMART: SM00237; Calx_beta; 2.			
DR	TIGRfams: TIGR00845; caca; 1.			
Q	SEQUENCE 928 AA; 102943 MW; A36BB30EE4123C0 CRC64;			

Query Match	95.1%;	Score 4563.5;	DB 11;	Length 928;
Best Local Similarity	94.2%;	Pred. No. 0;		
Matches 874;	Conservative 21;	Mismatches 26;	Indels 7;	Gaps 11.

Qy	1	MAMRLQJLTAFLHFGJLVTFVFLNCLRRADAGSSGVPSPRGONNECCSSSSPOCKEYIL	60
Db	1	MAMRLQJLTAFLHFGJLVTFVFLNCLRRADAGSGVPSAQNNECCSSSSPOCKEYIL	60
Qy	61	PIWPEBNSLQDKIARVIVYFVALIYMFELGVSIIDRPFMASIEVYTSQREYVITIKRNGE	120
Db	61	PIWPEBNSLQDKIARVIVYFVALIYMFELGVSIIDRPFMASIEVYTSQREYVITIKRNGE	120
Qy	121	TSTTIRVWNETSVNLTLMALGSSAPETLSLIEVCGHGFAGLDGSTTVGSAAFMF1	180
Db	121	TSTTIRVWNETSVNLTLMALGSSAPETLSLIEVCGHGFAGLDGSTTVGSAAFMF1	180
Qy	181	IIGICVUYIPDGETRKIKNLFVEFIITAAWSIFAYITWYMLAAVSPGVQVWMEGLTLTF	240
Db	181	IIGICVUYIPDGETRKIKNLFVEFIITAAWSIFAYITWYMLAAVSPGVQVWMEGLTLTF	240
Qy	241	FPPVCULLAMVADKRLLEFKYUHNKKYRDKNKGIIIEFGSHPRKGIEMDKKMMNSHFLDGN	300
Db	241	FPPVCULLAMVADKRLLEFKYUHNKKYRDKNKGIIIEFGSHPRKGIEMDKKMMNSHFLDGN	300

0Y	301	LVPLEGKRVDESSRRMRILKLDKQNHPEKDDLVEMANYALASHOOKSRAFRIOATR	360
Dd	301	FTPLEGKRVDESSRRMRILKLDKQNHPEKDDLVEMANYALASHOOKSRAFRIOATR	360
0Y	361	MMTGAGNLKFKHAAEOAKKASSKSEVHHDDEDEISKYFPEPCSYOCLEMGAVLLTVVR	420
Dd	361	MMTGAGNLKFKHAAEOAKKASSKSEVHHDDEDEISKYFPEPCSYOCLEMGAVLLTVVR	420
0Y	421	KGGDMSKTMYVDYKTEDGSANAGADYEETESTVYLKRGFTOKERSVGIIDDDIFEEDEHF	480
Dd	421	KGGDMSKTMYVDYKTEDGSANAGADYEETESTVYLKRGFTOKERSVGIIDDDIFEEDEHF	480
0Y	481	FVRLSNVTEIEEBOPEEGMPAIFNLSPLPRVNLVSPCAVATVLIIDDDHAGLFFPEECOTIH	540
Dd	481	FVRLSNVTEIEEBOPEEGMPAIFNLSPLPRVNLVSPCAVATVLIIDDDHAGLFFPEECOTIH	540
0Y	541	VSESIGVAEVAVLRTSGARGVAVIPFRIVESTAAGGEDEEDTYGELEFRNDETVKTRY	600
Dd	541	VSESIGVAEVAVLRTSGARGVAVIPFRIVESTAAGGEDEEDTYGELEFRNDETVKTRY	600
0Y	601	KIVDEEELERODNPFIALGEPKMERGIS-----DYDRLKLTMEEBEAKRIAEMKPV	653
Dd	601	KIVDRAEKAKKNVYIEMMGPRVDMSQKALLSPETDRKLVEEBEAKRIAEMKPV	660
0Y	654	IGEHPRKLEVIIIEESYEKFTYDKLIKTKTNLAVGTSMRDQFMEATITVSAGDEDEDES	713
Dd	661	IGEHPRKLEVIIIEESYEKFTYDKLIKTKTNLAVGTSMRDQFMEATITVSAGDEDEDES	720
0Y	714	GEERLPCSFEDYVMEFLVFNKVLFCACPPEYECGMACFAVSILIIIGMLTAITIGDLSHF	773
Dd	721	GEERLPCSFEDYVMEFLVFNKVLFCACPPEYECGMACFAVSILIIIGMLTAITIGDLSHF	780
0Y	774	GCTILKKSVAVYVAVGTSVPPTPASKAALDDVYADASIGVNTSSNNVNFELGIGLA	833
Dd	781	GCTILKKSVAVYVAVGTSVPPTPASKAALDDVYADASIGVNTSSNNVNFELGIGLA	840
0Y	834	MSVAIYWAOGOEHFHSAGTLAESVTLFTTIFAFVCISVLLYRRRPHLGGELGPRCKL	893
Dd	841	MSVAIYWAOMGOEHFHSAGTLAESVTLFTTIFAFVCISVLLYRRRPHLGGELGPRCKL	900
0Y	894	ATTWLFVSLMLLTXILFATLEAVCYIKGP	921
Dd	901	ATTWLFVSLMLLTXILFATLEAVCYIKGP	928

## RESULT 4

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ID      097801;          PRELIMINARY;          PRT;          934 AA.
AC      097801;
AD
DT      01-MAY-1999 (TREMBLrel. 10, Created)
DT      01-MAY-1999 (TREMBLrel. 10, last sequence update)
DT      01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE      Sodium-calcium exchanger isoform NCX1.3.
GN      NCX1.
OS      Macaca mulatta (Rhesus macaque) .
OC      Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC      Cercopithecinae; Macaca.
OX      NCBI_TaxID=9544;
RN      (1)
RP      SEQUENCE FROM N.A.
RC      TISSUE=KIDNEY;
RX      MEDLINE=99175198; PubMed=10075718;
RA      Li X.F., Lytton J.;
RL      "A circularized sodium-calcium exchanger exon 2 transcript.";
RL      J. Biol. Chem. 274:8153-8160(1999).
DR      EMBL; AF107593; AAD04173.1; -.
DR      InterPro: IPR003644; Calx.Beta.
DR      InterPro: IPR001623; DnaJ N.
DR      InterPro: IPR004837; Naca_Exmemb.
DR      InterPro: IPR004836; Na_Ca_Ex.
DR      Pfam; PF03160; Calx.Beta; 2.
DR      Pfam; PF01699; Na_Ca_Ex; 2.

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DR PRINTS: PRO1259; NACAEXCHNGR.  
DR SMART; SM00237; Calx\_beta; 2.  
DR TIGRFAMS; TIGR00845; caca; 1.  
DR PROSITE; PS50076; DNAJ\_2; 1.  
SQ SEQUENCE 934 AA; 104331 MW; 2A28DA30254BBC2 CRC64;

Query Match 72.1%; Score 3458.5; DB 6; Length 934;  
Best Local Similarity 71.8%; Pred. No. 3.1e-244;  
Matches 676; Conservative 108; Mismatches 129; Indels 29; Gaps 10;

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QY 1 MAMLRLOPLTSAFLHFGVLFVLF--LNGLRARAGSGSDVPSTGONNESCSSDCKEGV 58
DB 1 MRLSLSPFTSMGPHLLVYALFVSHVDYIALTEMBEGENETGE---CTGSYCKKGV 56
QY ILPIWYENPSLGDKTARVIVFVALIYMLGYSIADREMASIEVTSQERVTIKKP 118
DB 57 ILPIWEPQDPSFGDKIARAVIVFVAMVYMLGSIADRMSSIEVTSQEKITIKKP 116
QY 119 GFTSTTIRVWNETVSNLTMLAGSSAPETLLSLEVCGHGTAGDLGPSTIVGSAFNM 178
DB 117 GFTTKTVIRWNETVSNLTMLAGSSAPETLLSLEVCGHGTAGDLGPSTIVGSAFNM 176
QY 179 FLIIGCVVYIPDGETRKIKHLRVFTTAMSTFAYITMLIYMLAVSPGVYVWEGILTL 238
DB 177 FLIILCVVYVPPDGETRKIKHLRVFTTAMSTFAYITMLIYMLAVSPGVYVWEGILTL 236
QY 239 FFPVVCVLLAVNADKRLLEYKMKKRYRTDKHNGIIEETGDPHKG--IEMDKMMNSH 295
DB 237 FFPICVVFVAVNADRLLEYKMKKRYRTDKHNGIIEETGDPHKG--IEMDKMMNSH 296
QY 296 ---FLDGNLVPLEGKEYD---ESRREMRILKDLKOKHPEKOLDOLVEMANYALSHQ 348
DB 297 VENFLGALV-LEVDERDODDEARREMAIILKELKOKHPEKEIEQLIELANQVLSQQ 355
QY 349 KSRAPYRIQATRYMTAGNLTLLKHAQAQAKKASMSGVHDEPE-DEISVFEPPCSYOC 407
DB 356 KSRAPYRIQATRYMTAGNLTLLKHAQAQAKKASMSGVHDEPE-DEISVFEPPCSYOC 415
QY 408 LENCAGVALLTVNRKGGDMSTKTVDYKTEDGSANAGADYEFTGTVLKGFEQFSYV 467
DB 416 LENCAGVALLTVNRKGGDMSTKTVDYKTEDGSANAGADYEFTGTVLKGFEQFSYV 475
QY 468 IIDDIFEEDEHNFVRLSNVRIEEOPEECMPAIFNSLPPLPRAVLASPCVATVTLDD 527
DB 476 IIDDIFEEDEHNFVRLSNVRIEEOPEECMPAIFNSLPPLPRAVLASPCVATVTLDD 532
QY 528 HAGIIFEECDTIVSSSIGMEYKVLRTSGARCTVIVPFTVSGTAKGGEDEEDYTGEL 587
DB 533 HAGIIFEECDTIVSSSIGMEYKVLRTSGARCTVIVPFTVSGTAKGGEDEEDYTGEL 592
QY 588 EFNDETAVKTIIRKIVDEEYERQENEFIALGPKMMERG-----ISDVTDRK-LTME 639
DB 593 EFNDETAVKTIIRKIVDEEYERQENEFIALGPKMMERG-----ISDVTDRK-LTME 652
QY 640 EEBAKRIAEKQPVLCGHPKLEVIIEESYEKTTVDKLIKTNLALVGTSHRDOFMEA 699
DB 653 EEBERIRIAEGRPILEGHTKLEVIIEESYEKTTVDKLIKTNLALVGTSHRDOFMEA 712
QY 700 ITVSAAGDEDEDESGEERLPSCFDYVMHFLTVMKVLFLACVPRTYCHGACAVSILTI 759
DB 713 ITVSAAGDEDEDESGEERLPSCFDYVMHFLTVMKVLFLACVPRTYCHGACAVSILTI 772
QY 760 GMLTAIIGDLASHFGCTIGLKDVTAVVFAVFGTSPDPFASKAALODVYASIGNTY 819
DB 773 GMLTAIIGDLASHFGCTIGLKDVTAVVFAVFGTSPDPFASKAALODVYASIGNTY 832
QY 820 GSAVAVNVLGIGLAVSVAALYALOGOEHFVHSAAGTLAFSVTLFTIFAFVCISVLYRRR 879
DB 833 GSAVAVNVLGIGLAVSVAALYALOGOEHFVHSAAGTLAFSVTLFTIFAFVCISVLYRRR 892
QY 880 HLGSELGPRGCKLATVWLFVSLMLYILFATLEATCYIKGF 921
DB 893 ELIGELGPRGCKLATVWLFVSLMLYILFATLEATCYIKGF 934
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RESULT 5
ID 028662 PRELIMINARY; PRT; 941 AA.
AC 028662;
DT 01-NOV-1996 (TREMBlrel, 01, Created)
DT 01-NOV-1996 (TREMBlrel, 01, Last sequence update)
DT 01-JUN-2002 (TREMBlrel, 21, Last annotation update)
DE Renal Na/Ca exchanger NACA-2.
GN NCA1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX MEDLINE=92321271; PubMed=1621815;
RA Reilly R.F., Shugrue C.A.;
RT "cDNA cloning of a renal Na(+)-Ca2+ exchanger.";
RL Am. J. Physiol. 262:F1105-F1109(1992).
RN 12
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Reilly R.F., Shugrue C.A.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U52665; AAA97928.1;
DR InterPro: IPR003644; Calx_beta.
DR InterPro: IPR001623; Dnal_N.
DR InterPro: IPR004837; Naca_Exmemb.
DR InterPro: IPR004836; Na_Ca_Ex.
DR Pfam: PF03160; Calx_beta; 2.
DR Pfam: PF01699; Na_Ca_Ex; 2.
DR PRINTS: PRO1259; NACAEXCHNGR.
DR SMART; SM00237; Calx_beta; 2.
DR TIGRFAMS; TIGR00845; caca; 1.
DR PROSITE; PS50076; DNAJ_2; 1.
SQ SEQUENCE 941 AA; 105128 MW; 7E11396DE70A4084 CRC64;

Query Match 71.8%; Score 3442.5; DB 6; Length 941;
Best Local Similarity 71.1%; Pred. No. 4.7e-243;
Matches 669; Conservative 109; Mismatches 128; Indels 35; Gaps 10;

QY 8 PLTSAFLHFGVLFVLF--LNGLRARAGSGSDVPSTGONNESCSSDCKEGVILPIWY 66
DB 9 PLTSMGHLAIVALEFFRRDHSVSAETEMEGENETGE---CTGSYCKKGVILPIW 64
QY 67 NPSLGDKIARVIVFVALIYMLGYSIADREMASIEVTSQERVTIKKPNGESTTTI 126
DB 65 DPSFGDKIARAVIVFVAMVYMLGYSIADRMSSIEVTSQEKITIKKPNGETTKTV 124
QY 127 RVWNETVSNLTMLAGSSAPETLLSLEVCGHGTAGDLGPSTIVGSAFNMFTITGIV 186
DB 125 RVWNETVSNLTMLAGSSAPETLLSLEVCGHGTAGDLGPSTIVGSAFNMFTITGIV 184
QY 187 YVLPDETRKIKHLRVFTTAMSTFAYITMLIYMLAVSPGVYVWEGILTFEPPCVL 246
DB 185 YVLPDETRKIKHLRVFTTAMSTFAYITMLIYMLAVSPGVYVWEGILTFEPPCVL 244
QY 247 LAMVADKRLLEYKMKKRYRTDKHNGIIEETGDPHKG--IEMDKMMNSH--FLDGN 300
DB 245 LAMVADKRLLEYKMKKRYRTDKHNGIIEETGDPHKG--IEMDKMMNSH--FLDGN 304
QY 301 LVPLEKEYD---ESRREMRILKDLKOKHPEKOLDOLVEMANYALSHQKSRAPYRI 356
DB 305 LVPLEKEYD---ESRREMRILKDLKOKHPEKOLDOLVEMANYALSHQKSRAPYRI 363
QY 357 OATRYMTAGNLTLLKHAQAQAKKASMSGVHDEPE-DEISVFEPPCSYOCLENGAVL 415
DB 364 OATRYMTAGNLTLLKHAQAQAKKASMSGVHDEPE-DEISVFEPPCSYOCLENGAVL 423
QY 416 LTVNRKGGDMSTKTVDYKTEDGSANAGADYEFTGTVLKGFEQFSYVGIIDDIFE 475
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Db 424 LTIIRGGDLNITVFDVFRPREDGFGANNQSDYEFTEGIVVFKPBGTOKEINVGIIIDDDIFE 483
Qy 476 EDEHFVFKLSNVRIEEOPEEGMPAIFNSLPLERAVLASPCVATVITLDDHAGITFEF 535
Db 484 EDENFVLVLSNVKVSSETSSEJGLEAHNHIS--"TLACIGSPCTATVITFPDDHAGITFEF 540
Qy 536 CDTIHVSISIGVMBVXVUTRSNGAGYIVPRVRYEGAKAGGDEFEETVTELEKNDETY 555
Db 541 ESVTHVSISIGIMVKKVLTIRTSNGANNIVPKKITEGTARGGDEFEETGCELEFONDEIV 600
Qy 596 KTIIRKIVDEEYEROEENFIATLCEPKMMERG-----ISDVYDRK--LTJME 640
Db 601 KIITIRIFRDREYREKESLSVLEEPKIRMGKALLNELGFTTIEEYDOKOPLTSKE 660
Qy 661 EBAKRIAEMGKPVJGHEHPKLEVIIIEESYEKTTVDKLIKTKNTLALVYGTSHMRDQMEAT 700
Db 661 EEBERRIEMGPRJIGEHKTELVIIIEESYEFKSTYDKLIKTKNTLALVGTSMRQFTEAI 720
Qy 701 TVSAAGDEDEEESGEBERPSCEQDVMHFVMEKVLVACVPRPEYCHGMACFANSLITG 760
Db 721 TVTSGEDDDDECEBEKIPSCFQDVHMFVLVFMKVLVAFAPPEYVWGMACFVITSLIMIG 780
Qy 761 MLTAIIGDLASHFCCTIGLKDSDVAVVVFAVFGTSVPDPTFASKAALODVYADASIGNVTG 820
Db 781 LTLTAFIGDLASHFCCTIGLKDSVAVVFAVVALGTSVPTDPTFASKVAALODQYADASIGNVTG 840
Qy 821 SNAVNVFJGIGLANSVAAIYVALOGQEFHVSAGTLAFSVLTFTTFAVCJISVLLYRRRH 880
Db 841 SNAVNVFJGIGVANSIAIYHANAENGHEHKVSPGTLASVLTFTTFAFVINGVLLYRRPE 900
Qy 881 LGGELGGRGCKLAPTMVLFVSLMLTYITFAFLEAVCYIKRG 921
Db 901 IGGELGGRKAKLITSCLEFVLLMLTYITFESSLEAVYCHIRG 941

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RESULT 6
097514 ID Q9TSL4 PRELIMINARY; . PRT; 941 AA.
AC Q9TSL4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Na/Ca exchanger Isoform NACA6.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
XC NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94148976; PubMed=8106495;
RA Kofuji P., Lederer W.J., Schulze D.H.;
RT "Mutually exclusive and cassette exons underlie alternatively spliced
RL isoforms of the Na/Ca exchanger." ;
J. Biol. Chem. 269:5145-5149(1994).
DR InterPro: IPR003644; Calx_beta.
DR InterPro: IPR001623; DnaJ_N.
DR InterPro: IPR004837; Naca_Exemb.
DR InterPro: IPR004836; Na_Ca_Ex.
DR Pfam: PF03160; Calx-beta; 2.
DR Pfam: PF01699; Na_Ca_Ex; 2.
DR PRINTS: PRO1259; NACAEXCHNGR.
DR SMART: SM00237; Calx_beta; 2.
DR TIGRFAMs: TIGR00845; caca; 1.
DR PROSITE: PS50076; DNAJ_2; 1.
SQ SEQUENCE 941 AA; 104995 MW; AEC76774E9E81815 CRC64;

Query Match 71.7%; Score 3437.5; DB 6; Length 941;
Best Local Similarity 71.0%; Pred.No.1.le-24;
Matches 669; Conservative 111; Mismatches 125; Indels 37; Gaps 11.

      8 PLTSFLHGLTVFLV-F-LNGLRAERAGSGDVPSTGQNNSSCGSSDDCKEGEVILPIWPE 66
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

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Dd	9	PFSGHFLIALVALPFPRVDHVSAREMEBGEGNTEG----	CTGSYVCKRGVILPIMEQ	64
Qy	67	NPSTGDKIARVIVYFVALIYMFVLSIADPRMASEIYTSOEUEVTIKRPNGETSTTTI	12	
Dd	65	DPSPGDKIARATVYFVAAMYMFVLSIADPRMSSIEVITSOEKEITIKR-NGETTKTV	12	
Qy	127	RYNNEYVSNLTMAALSSAPELLISLIEVCGGFIAGDIPSTVYSAANMFIITIGIV	18	
Dd	124	RIMNEYVSNLTMAALSSAPELLISLIEVCGHNFAGDLGISTVYSAANMFIITIALCV	18	
Qy	187	YVINDGETRKIKHLRFEFTTAAMSIFAYIWMILIAVSPCVQVMGELTLTFEPVCLV	24	
Dd	184	YVVDGSTRKIKHLRFEFTTAAMSIFATWILXIIISVSPQIVEMGELTLTFEPFICV	24	
Qy	247	LAWVADKRLLEFYKMKKRYRTDKHNGIILIEEGDHPKG--IEMGKMNSH--FLDGN	30	
Dd	244	FAMVADKRLLEFYKYVKRYRACKQGMIIIEHGEDRPSSTKTEIEMDGKVYNSHYNFLDA	30	
Qy	301	LVPLEGKEND---EERREMILINDKQKHENKODLVJAMVAYVALSHNOOKSRAPFYI	35	
Dd	304	LV-LDVERODDEEARREARLELQKQKPEKTEIOLIELANVOVLS00QSRAPFYI	36	
Qy	357	QATPMKMGANIILKIKRAAQAKASSMEVHDEBE-DFISKVFEDCSQOCLENGAVL	41	
Dd	363	QATPMKMGANIILKIKRAAQAKASMHVNTNEMANDPVSKIFFEBOGTQOCLENGTYA	42	
Qy	416	LTVVRKGGMSKMTVYDYKTEDGSANAGADVEFTGTVLKGETOKEFSVGIIDDIIE	47	
Dd	423	LTVVRKGGMSKMTVYDYKTEDGSANAGADVEFTGTVLKGETOKEIRNGIIDIIDE	48	
Qy	476	EDHEFFARLSNVNILEEOEBEGMPRAIFNSLPLPAVALASCVAVTYIIDDHAGIFTE	53	
Dd	483	EDENFVLHLSNVVVSSETSEBDGILENNHS--TLACGSCVTYVYIIPDDHAGIFTE	53	
Qy	536	CDTLHVSSEISGVMEVYVLTSTSGARGVLYPFRFVETGAKGGEDEDTYELFEKNDVY	59	
Dd	540	ESYVHSESGIMDEKVLKRSKARGVLYPYRTIGTARGGEDP EDTGCELEFONDEY	59	
Qy	596	KTIKRVKIVDEEYERODENFFIALGEPKWMERG-----ISDVTDRK--LJME	63	
Dd	600	KTISVYKVIDDEYERKNTFLEIGEBRLVEMSEKALLINELGFTITEYDOKPLTSK	65	
Qy	640	EEBKRIAEKGVLEGEHKEVLIIEESIEFTYVDKLIKRTNALVYGHSHRODPEA	69	
Dd	660	EEEBRRIAEGRPILEBHTKLEVIIEESYEFKSTYDKLIKRTNALVYGHSHRODPEA	71	
Qy	700	ITVSAADDEDSDSGEERTPSCPDVYMHFLTYEMKVLFACPRPTEYCHGACFVSLII	75	
Dd	720	ITVSAADDEDSDSGEERTPSCPDVYMHFLTYEMKVLFACPRPTEYVNGACFVSLI	77	
Qy	760	GMLTAIIGDLSHFPGCTIGLKSQVTAVFAVARGTSVPTFPFASKAALADODYADASIGNY	81	
Dd	780	GLTLAIFGDLASHFGCTIGLKSQVTAVFAVARGTSVPTFPFASKAALADODYADASIGNY	83	
Qy	820	GSNAVNVFLIGLAMSVAALYMALOGEHFHSAGTLASVYTLFTIFAPVCIISVLYRRP	87	
Dd	840	GSNAVNVFLIGLAMSVAALYMAHANGHEHKVSPGTLASVYTLFTIFAFINVGVLVRRP	89	
Qy	880	HJGELGGRPGCKIATWVLSVJMLIXILFAPLAEVYCKIRGF	92	
Dd	900	EIGELGGRPRAKULITSCLEFVLMWLIYFSSLELVYCHIRGF	94	

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RESULT 7
Q9R238
ID Q9R238 PRELIMINARY; PRT; 934 AA.
AC Q9R238;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Na+/Ca2+-exchanging protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DAHL/RAP R SPRAGUE-DAWLEY;  
 RA Unlap M.T., Bell P.D.;  
 RT "cDNA cloning of two Na<sup>+</sup>/Ca<sup>2+</sup> exchangers in mesangial cells from Dahl/Rapp salt-sensitive (S) and salt-resistant (R) rats."  
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF109163; AAD23386.1; -  
 DR InterPro: IPR003644; Calx\_beta.  
 DR InterPro: IPR001623; DnaJ\_N.  
 DR InterPro: IPR004837; NaCa\_Exmemb.  
 DR InterPro: IPR004836; Na\_Ca\_Ex.  
 DR Pfam: PF03160; Calx\_beta; 2.  
 DR Pfam: PF01699; Na\_Ca\_Ex; 2.  
 DR PRINTS: PR01259; NACAEXCHNGR.  
 DR SMART: SM00237; Calx\_beta; 2.  
 DR TIGRFRAMS: TIGR00845; caca; 1.  
 DR PROSITE: PS50076; DNaJ\_2; 1.  
 SQ SEQUENCE 934 AA; 104166 MW; C04ED08A75633DDC CRC64;

Query Match 71.5%; Score 3427.5; DB 11; Length 934;  
 Best Local Similarity 70.9%; Pred. No. 5.8e-242;  
 Matches 671; Conservative 107; Mismatches 127; Indels 41; Gaps 11;

OY 4 LRLQPLTSAPLHFGVLTFLVFL-----NGLRAGSGSDVPSTGQNNESCGSSDCK 55  
 DB 2 LRLSLPPNVSMGRLVLTVALFTLHVDTADTAEATGCGN-----ETTECTGSYYCK 53  
 OY 56 EGVILPTWYENPNSLGGKIRARIVYFVALYMLGVSIIADREMASTEVITSGREVTIK 115  
 DB 54 KGVILPTWEPDPSFGGKIRARATVYFVAAYMYMFLGVSIIADREMASTEVITSGREVTIK 113  
 OY 116 KPNGETSTTIRVWNEVSNLTLMALGSSAPETILSLIEVCGHGTAGDGPSTVGSAA 175  
 DB 114 KPNGETTKTVIRWNEVSNLTLMALGSSAPETILSLIEVCGHGTAGDGPSTVGSAA 173  
 OY 176 FNMFIIGICVYVDPGETRKIKHLRVFTTAAMSIFAYIMLYMILAVFSPGVQWEG 235  
 DB 174 FNMFIIALCVYVDPGETRKIKHLRVFTTAAMSIFAYIMLYMILAVFSPGVQWEG 233  
 OY 236 LTLFFPVCVLLAVADKRLLFYKMKKRTDKHKGIIITEGDHPKG---IEMDGKMM 292  
 DB 234 LTLFFFPICVFAVADKRLLFYKMKKRTDKHKGIIITEGDHPKG---IEMDGKMM 293  
 OY 293 NSH---FLDGLNVLLEGKEVD---ESRREIRILKDKLKHPEKXLDOLVEMANYYALS 345  
 DB 294 NSHVDNFDLGLALV-LEVDERQDDEEAKREMARILKELKHPEKXLDOLVEMANYYALS 352  
 Y 346 HOKSRAFYRIQATRMGTAGNLTAKHAADCAKASSMSVHTDEPE-DEISKVFFDPDS 404  
 DB 353 OOKSRAFYRIQATRMGTAGNLTAKHAADCAKASSMSVHTDEPE-DEISKVFFDPDS 412  
 OY 405 YOCLENGAVLLVYKRGKMSKTYDYTKEDGSANAGADYEFTBSTVYLKPGETOKEF 464  
 DB 413 YOCLENGCTAALTIIRRGGLTNTVSYDFTEDGTANAGSDYEFTBSTVYLKPGETOKEI 472  
 OY 465 SVGLIIDDIFEEDEHFFVRLSNVRIEEDPECEGMPAIFNSLPLR-AVLASPCVAATVI 523  
 DB 473 RVGLIIDDIFEEDEHFFVRLSNVRIEEDPECEGMPAIFNSLPLR-AVLASPCVAATVI 528  
 OY 524 LDDDHAGIFTECDTIVHSESIGMEYKVTSGARGTIVPFRFTVGTAKGGEDEEDT 583  
 DB 529 FDDDHAGIFTECDTIVHSESIGMEYKVTSGARGTIVPFRFTVGTAKGGEDEEDT 588  
 OY 584 YGELFENADETVTKIRKIVDEEYERQENFIALGCPKMMERGI-----SDVTDK- 635  
 DB 589 CGELFENADETVTKIRKIVDEEYERQENFIALGCPKMMERGI-----SDVTDK- 648  
 OY 636 LTHBEEAKKIAEMKGVNGLSEHRLKLEVIITSESEFETTVYKLIKTNLALVGTSHSRDQ 695  
 DB 649 LTHBEEAKKIAEMKGVNGLSEHRLKLEVIITSESEFETTVYKLIKTNLALVGTSHSRDQ 708

OY 696 FMEATVSAAGDEDEDESGERLPSCFDYVMHFLTVMKVLFAVCVPPTEXCHMGACPAVS 755  
 DB 709 FIEATVSAAGDEDDDCGEGEKLPSCFDYVMHFLTVMKVLFAVCVPPTEXCHMGACPAVS 768  
 OY 756 ILIIGMTAIIIGDLASHFGCTIGLKDSVTVAVFACTSVPDFTFASAAALDQYADAST 815  
 DB 769 ILMIGLITTAIGDLASHFGCTIGLKDSVTVAVFACTSVPDFTFASAAALDQYADAST 828  
 OY 816 GNTGSAVAVVFGIGLAWGVAAYMALOGEEFVSAAGTAAFSVTLPTTIFAFCISVLLY 875  
 DB 829 GNTGSAVAVVFGIGLAWGVAAYMALOGEEFVSAAGTAAFSVTLPTTIFAFCISVLLY 888  
 OY 876 RRRHELGLGEGRPGCKLATWTLFVSLMLYLIFATLEAYCYIKGF 921  
 DB 889 RRRHELGLGEGRPGCKLATWTLFVSLMLYLIFATLEAYCYIKGF 934

RESULT 8  
 Q9WU30 PRELIMINARY; PRT; 934 AA.  
 ID Q9WU30;  
 AC Q9WU30;  
 DT 01-NOV-1999 (TREMURel. 12, Created)  
 DT 01-NOV-1999 (TREMURel. 12, Last sequence update)  
 DT 01-JUN-2002 (TREMURel. 21, Last annotation update)  
 DE Na<sup>+</sup>/Ca<sup>2+</sup>-exchanging protein.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY;  
 RA Unlap M.T., Bell P.D.;  
 RT "cDNA cloning of two Na<sup>+</sup>/Ca<sup>2+</sup> exchangers in mesangial cells from Dahl/Rapp salt-sensitive (S) and salt-resistant (R) rats."  
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF109166; AAD23389.1; -  
 DR InterPro: IPR003644; Calx\_beta.  
 DR InterPro: IPR001623; DnaJ\_N.  
 DR InterPro: IPR004837; NaCa\_Exmemb.  
 DR InterPro: IPR004836; Na\_Ca\_Ex.  
 DR Pfam: PF03160; Calx\_beta; 2.  
 DR Pfam: PF01699; Na\_Ca\_Ex; 2.  
 DR PRINTS: PR01259; NACAEXCHNGR.  
 DR SMART: SM00237; Calx\_beta; 2.  
 DR TIGRFRAMS: TIGR00845; caca; 1.  
 DR PROSITE: PS50076; DNaJ\_2; 1.  
 SQ SEQUENCE 934 AA; 104210 MW; 054D06E9179098B5 CRC64;

Query Match 71.4%; Score 3425.5; DB 11; Length 934;  
 Best Local Similarity 70.8%; Pred. No. 8.2e-242;  
 Matches 670; Conservative 108; Mismatches 127; Indels 41; Gaps 11;

OY 4 LRLQPLTSAPLHFGVLTFLVFL-----NGLRAGSGSDVPSTGQNNESCGSSDCK 55  
 DB 2 LRLSLPPNVSMGRLVLTVALFTLHVDTADTAEATGCGN-----ETTECTGSYYCK 53  
 OY 56 EGVILPTWYENPNSLGGKIRARIVYFVALYMLGVSIIADREMASTEVITSGREVTIK 115  
 DB 54 KGVILPTWEPDPSFGGKIRARATVYFVAAYMYMFLGVSIIADREMASTEVITSGREVTIK 113  
 OY 116 KPNGETSTTIRVWNEVSNLTLMALGSSAPETILSLIEVCGHGTAGDGPSTVGSAA 175  
 DB 114 KPNGETTKTVIRWNEVSNLTLMALGSSAPETILSLIEVCGHGTAGDGPSTVGSAA 173  
 OY 176 FNMFIIGICVYVDPGETRKIKHLRVFTTAAMSIFAYIMLYMILAVFSPGVQWEG 235  
 DB 174 FNMFIIALCVYVDPGETRKIKHLRVFTTAAMSIFAYIMLYMILAVFSPGVQWEG 233  
 OY 236 LTLFFPVCVLLAVADKRLLFYKMKKRTDKHKGIIITEGDHPKG---IEMDGKMM 292  
 DB 234 LTLFFFPICVFAVADKRLLFYKMKKRTDKHKGIIITEGDHPKG---IEMDGKMM 293



233 NSH---FLDGNLVPLEGEVD-----ESRREMIIRILKDKQKHPKEDLDOLVEMANYALS 345  
294 NSHVNFDLGDALV-LEVERDODDDEARREMARILKELKOKPKDPEIDELILANYALS 352  
346 HOOKSRAFYRIQATRMGTGAGNILKHAEOAKKASMSSEVHTDEPE-DFISKVEFDPDS 404  
353 OOKSRAFYRIQATRMGTGAGNILKHAEOAKKASMSSEVHTDEPE-DFISKVEFDPDS 412  
405 YOCLENCAGVLLTVYRKGGDMKMTYVDKTTEDGSANAGADVEFTGYVLLKPGETQKFE 464  
413 YOCLENCAGVLLTVYRKGGDMKMTYVDKTTEDGSANAGADVEFTGYVLLKPGETQKFE 472  
465 SVGIIDDDIIFEEDEHFFLVLSNVRIEEOPEEGMPAIPNSIPLPR-AVLASPCVATYTI 523  
473 RYGIIDDDIIFEEDEHFFLVLSNVRIEEOPEEGMPAIPNSIPLPR-AVLASPCVATYTI 528  
524 LDDHAGIIFTEECDTIHVSESIGVMEVKVLTSGAGTVIYVPTVEGTAKGGEDFEDT 583  
529 FDDHAGIIFTEECDTIHVSESIGVMEVKVLTSGAGTVIYVPTVEGTAKGGEDFEDT 588  
584 YGELEFKNDEYKTRVKIVDEEYERQENFIALGEPKWMERG-----SDVTDK- 635  
589 CGELEFQNDIYKTRIRIFDREYEKECSFSLVEEPEKWMIRGKMGGETLLEEDDKOP 648  
636 LIMEEERKRIAEKMPVLEGEHPLKLEVIIESEYEFTYVDKLIKPTNLALVYGTSMRO 695  
649 LTSKEEERRIAEKMPVLEGEHPLKLEVIIESEYEFTYVDKLIKPTNLALVYGTSMRO 708  
696 FMEATVSAAGDEDESEGERLPSCFDYVMHFLTVFMKVLFCVYPTVEGTAKGGEDFEDT 755  
709 FFEATVSAAGDEDESEGERLPSCFDYVMHFLTVFMKVLFCVYPTVEGTAKGGEDFEDT 768  
756 IITIMLTAIIGDLSHSCCTIGLKDSTAVVFAFGTSVPTFRASKAALADYVADASI 815  
769 ILMILTAIIGDLSHSCCTIGLKDSTAVVFAFGTSVPTFRASKAALADYVADASI 828  
816 GNVTSNANVNFVIGLGSVAIYALOGGEHVSAGTGLASVLTFTFAVCISVLLY 875  
829 GNVTSNANVNFVIGLGSVAIYALOGGEHVSAGTGLASVLTFTFAVCISVLLY 888  
876 RRRPHLGGELGPRCKLATWLVFVSLWLLYLFATLEAYCYIKGF 921  
889 RRRPHLGGELGPRCKLATWLVFVSLWLLYLFATLEAYCYIKGF 934

RESULT 9  
Q9R239 PRELIMINARY: PRT: 957 AA.

AC Q9R239: 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
DE Na+/Ca2+-exchanging protein.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
NCBI\_TaxID=10116;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=DAHL/RAP S SPRAGUE-DAWLEY;  
RA Unlap M.T., Bell P.D.;  
RT "cDNA cloning of two Na+/Ca2+ exchangers in mesangial cells from  
RT Dahl/Rap salt-sensitive (S) and salt-resistant (R) rats.";  
RL Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF109164; AAD3387.1;  
DR InterPro: IPR003644; Calx beta.  
DR InterPro: IPR001623; Dnal\_N.  
DR InterPro: IPR004837; Naca\_Exmemb.  
DR InterPro: IPR004836; Na\_Ca\_Ex.  
DR Pfam: PF01699; Na\_Ca\_Ex; 2.  
DR PRINTS: PR01259; NACAEXCHNGR.

DR SMART: SM00237; Calx beta; 2.  
DR TIGRfams: TIGR00845; caca; 1.  
DR PROSITE: PS00076; Dnal\_2; 1.  
SQ SEQUENCE 957 AA; 106724 MW; 7A146630451EAA7E CRC64;

Query Match 71.2%; Score 3417; DB 11; Length 957;  
Best Local Similarity 69.5%; Pred. No. 3.5e-241;  
Matches 673; Conservative 104; Mismatches 128; Indels 64; Gaps 11:

4 LRLQPLTSAFLEHFGVTVLFL-----NGLRADAGSGGVSTGQNNESGSSDCK 55  
2 LRLSPNPNVSMKGRVLTVALLEFTHVDITADTEAETGNN-----ETTECTGSYCK 53  
56 EGVIIPIWPEKPSGDKRARIYVFNALIVFLCVSTIADRFMSIEVTSQREVTIK 115  
54 KGVILPIWPEKPSGDKRARIYVFNALIVFLCVSTIADRFMSIEVTSQREVTIK 113  
116 KPNGETSTTIVVNETVSNLTLMALGSSAPRILSLIEVCGHGTACDLAGSTIVGSA 175  
114 KPNGETSTTIVVNETVSNLTLMALGSSAPRILSLIEVCGHGTACDLAGSTIVGSA 173  
176 FNMFTIIGICVYVYIDGETRKTIKHLRVEFTIAMSIFAYILYMLLAVFSPGVOWEGL 235  
174 FNMFTIIGICVYVYIDGETRKTIKHLRVEFTIAMSIFAYILYMLLAVFSPGVOWEGL 233  
236 LTLFEPVGVLLANVADRKLFLYKYMKKYRDKRGIIIEFDGPKG---IENDGKM 292  
234 LTLFEPVGVLLANVADRKLFLYKYMKKYRDKRGIIIEFDGPKG---IENDGKM 293  
293 NSH---FLDGNLVPLEGEVD-----ESRREMIIRILKDKQKHPKEDLDOLVEMANYALS 345  
294 NSHVNFDLGDALV-LEVERDODDDEARREMARILKELKOKPKDPEIDELILANYALS 352  
346 HOOKSRAFYRIQATRMGTGAGNILKHAEOAKKASMSSEVHTDEPE-DFISKVEFDPDS 404  
353 OOKSRAFYRIQATRMGTGAGNILKHAEOAKKASMSSEVHTDEPE-DFISKVEFDPDS 412  
405 YOCLENCAGVLLTVYRKGGDMKMTYVDKTTEDGSANAGADVEFTGYVLLKPGETQKFE 464  
413 YOCLENCAGVLLTVYRKGGDMKMTYVDKTTEDGSANAGADVEFTGYVLLKPGETQKFE 472  
465 SVGIIDDDIIFEEDEHFFLVLSNVRIEEOPEEGMPAIPNSIPLPR-AVLASPCVATYTI 523  
473 RYGIIDDDIIFEEDEHFFLVLSNVRIEEOPEEGMPAIPNSIPLPR-AVLASPCVATYTI 528  
524 LDDHAGIIFTEECDTIHVSESIGVMEVKVLTSGAGTVIYVPTVEGTAKGGEDFEDT 583  
529 FDDHAGIIFTEECDTIHVSESIGVMEVKVLTSGAGTVIYVPTVEGTAKGGEDFEDT 588  
584 YGELEFKNDEYKTRVKIVDEEYERQENFIALGEPKWMERG-----SDVTDK- 635  
589 CGELEFQNDIYKTRIRIFDREYEKECSFSLVEEPEKWMIRGKMGGETLLEEDDKOP 648  
636 LIMEEERKRIAEKMPVLEGEHPLKLEVIIESEYEFTYVDKLIKPTNLALVYGTSMRO 695  
649 LTSKEEERRIAEKMPVLEGEHPLKLEVIIESEYEFTYVDKLIKPTNLALVYGTSMRO 708  
696 FMEATVSAAGDEDESEGERLPSCFDYVMHFLTVFMKVLFCVYPTVEGTAKGGEDFEDT 755  
709 FFEATVSAAGDEDESEGERLPSCFDYVMHFLTVFMKVLFCVYPTVEGTAKGGEDFEDT 768  
756 IITIMLTAIIGDLSHSCCTIGLKDSTAVVFAFGTSVPTFRASKAALADYVADASI 815  
769 ILMILTAIIGDLSHSCCTIGLKDSTAVVFAFGTSVPTFRASKAALADYVADASI 828  
816 GNVTSNANVNFVIGLGSVAIYALOGGEHVSAGTGLASVLTFTFAVCISVLLY 875  
829 GNVTSNANVNFVIGLGSVAIYALOGGEHVSAGTGLASVLTFTFAVCISVLLY 888  
876 RRRPHLGGELGPRCKLATWLVFVSLWLLYLFATLEAYCYIKGF 921  
889 RRRPHLGGELGPRCKLATWLVFVSLWLLYLFATLEAYCYIKGF 934





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Db 2 LRLSLPWNVSMGFRVLTVALLFTVHDHTADTAEATGNN-----ETTECTGSYYCK 53
Qy 56 BEVILPIWPNPESLGDKARIATYFVALITYMFLGVSTIADRFMASIEVITSQEREVTIK 115
Db 54 KSVILPIWPNPESLGDKARIATYFVALITYMFLGVSTIADRFMASIEVITSQEREVTIK 113
Qy 116 KNGESTTTIWMNMTVSNLTLMALGSSAPETLSLIEVCHGFLAGDLSSTVIGSA 175
Db 114 KNGESTTTIWMNMTVSNLTLMALGSSAPETLSLIEVCHGFLAGDLSSTVIGSA 173
Qy 176 FMNFIIGICVYVVDGETRRIKHLRVEFTIAMSIFAYIMLMLAVSPGVQVWEGT 235
Db 174 FMNFIIGICVYVVDGETRRIKHLRVEFTIAMSIFAYIMLMLAVSPGVQVWEGT 233
Qy 236 LFLFPPPCVLLAMVADKLLTYKYMKKYRPDKHGIITIEEGHPKG---IENDGKMM 292
Db 234 LFLFPPPCVLLAMVADKLLTYKYMKKYRPDKHGIITIEEGHPKG---IENDGKMM 293
Qy 293 NSH---FLDGNLVLEGGKVD---ESRREMTRIKDLKQKHPEKDLDQVEMANYALS 345
Db 294 NSHVDNFDLGDALV-LEVDERRDODDEBARREMARILKELKQKHPEKDLDQVEMANYALS 352
Qy 346 HOOKSRAFYRIQATRMATGAGNILKKAEOAKKASMSSEVHTDEPE-DFISKVFPDPS 404
Db 353 OOKSRAFYRIQATRMATGAGNILKKAEOAKKASMSSEVHTDEPE-DFISKVFPDPS 412
Qy 405 YOCLEKCGAVLLTVARKGDMKTYVDYKTEGDSANAGADYEFTEGTVLKPGETQKEF 464
Db 413 YOCLEKCGAVLLTVARKGDMKTYVDYKTEGDSANAGADYEFTEGTVLKPGETQKEF 472
Qy 465 SVGIIDDDDFEEDHEFVLSNVRIEEOPEEGMPAIFNSJLPR-AVLASPCVATVI 523
Db 473 RGIIDDDDFEEDHEFVLSNVRIEEOPEEGMPAIFNSJLPR-AVLASPCVATVI 528
Qy 524 LDDHAGITFECDTIHVSSEIGVMEKVLRTSGARGTVIPRVEGTAKGGEDFEDT 583
Db 529 FDDHAGITFECDTIHVSSEIGVMEKVLRTSGARGTVIPRVEGTAKGGEDFEDT 588
Qy 584 YGELERKNDYKTIYKIVDEDEYERQENFALGEPKMMENG-----627
Db 589 CGELERKNDYKTIYKIVDEDEYERQENFALGEPKMMENG-----627
Qy 628 -----ISDVTDRK--LTMEEBAKRIAEMGKPYLGEPKL 660
Db 649 KMYGCPVPRKYNARHPITPSTYISISEYEDKQPLTSKEEBERKIAEMGKPYLGEPKL 708
Qy 661 EVIIESEYFEKTYVDKLIKLTNLALVVGTHSMEDQFMEALTVSACDEDEDESGBERLPS 720
Db 709 EVIIESEYFEKTYVDKLIKLTNLALVVGTHSMEDQFMEALTVSACDEDEDESGBERLPS 768
Qy 721 CDDYVNHFLTVMKVLFACVPRPEYCHGNACFVSTLIIGMLTAIIGDLASHGCTITGLK 780
Db 769 CDDYVNHFLTVMKVLFACVPRPEYCHGNACFVSTLIIGMLTAIIGDLASHGCTITGLK 828
Qy 781 DSVTAVVFAFGSVDPDTFASKAALADYADASIGNVTGSNAVNFELGIGLSAAVAY 840
Db 829 DSVTAVVFAFGSVDPDTFASKAALADYADASIGNVTGSNAVNFELGIGLSAAVAY 888
Qy 841 WALOGGEHVSAGTASFVTLFTTFAFVCSIVLLYRRRPHLGELGPGCKLATTWLEY 900
Db 889 HANGGEHVSAGTASFVTLFTTFAFVCSIVLLYRRRPHLGELGPGCKLATTWLEY 948
Qy 901 SIMLILITFATLEAYCYIKGF 921
Db 949 LMLLITFEFSSLEAYCHIKGF 969

RESULT 12
Q9PT19 PRELIMINARY: PRT; 968 AA.
AC Q9PT19: 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)

DE 01-JUN-2002 (Tremblrel. 21, last annotation update)
CN Cardiac sodium-calcium exchanger.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RA MEDLINE=99447215; PubMed=10516099;
RX Xue X.H., Hryshko L.V., Nicoll D.A., Philipson K.D., Tibbits G.F.;
RT "Cloning, expression, and characterization of the trout cardiac
RT Na(+)/Ca(2+) exchanger."
RL Am. J. Physiol. 277:C693-C700(1999).
DR EMBL; AF15313; AAC6363.1; -.
DR InterPro; IPR003644; Calx_beta.
DR InterPro; IPR004837; NaCa_Exmemb.
DR InterPro; IPR004836; NaCa_Ex.
DR Pfam; PF03160; Calx_beta; 2.
DR Pfam; PF01699; Na_Ca_Ex; 2.
DR PRINTS; PR01259; NACAEXCHNGR.
DR SMART; SM00237; Calx_beta; 2.
DR TIGRFAMs; TIGR00845; caca; 1.
SQ SEQUENCE 968 AA; 107504 MW; 5F8A92824B26DA36 CRC64;

Query Match 68.6%; Score 3990.5; DB 13; Length 968;
Best Local Similarity 66.2%; Pred. No. 6;e-233;
Matches 645; Conservative 121; Mismatches 135; Indels 73; Gaps 14;

Qy 10 TSAPLHFGI---VTFPLFLNGLRAGSGGDPSTNG-----ONNESC-SGSSDCKEYG 58
Db 6 TSFPLFCALQTLVLAFFSEIKFEVTAGNSN-PSLSTNSIGNQNKKDSVDTEKGVV 64
Qy 59 ILPIWPNPESLGDKARIATYFVALITYMFLGVSTIADRFMASIEVITSQEREVTIKPN 118
Db 65 ILPIWPNPESLGDKARIATYFVALITYMFLGVSTIADRFMASIEVITSQEREVTIKPN 124
Qy 119 GETSTTTIWMNMTVSNLTLMALGSSAPETLSLIEVCHGFLAGDLSSTVIGSA 178
Db 125 GEKVTITVIRNMTVSNLTLMALGSSAPETLSLIEVCHGFLAGDLSSTVIGSA 184
Qy 179 FTIIGICVYVVDGETRRIKHLRVEFTIAMSIFAYIMLMLAVSPGVQVWEGT 238
Db 185 FTIIGICVYVVDGETRRIKHLRVEFTIAMSIFAYIMLMLAVSPGVQVWEGT 244
Qy 239 FFPVVCVLLAMVADKLLTYKYMKKYRPDKHGIITIEEGD---HPKGIENDGKMMNS 294
Db 245 FFPVVCVLLAMVADKLLTYKYMKKYRPDKHGIITIEEGD---HPKGIENDGKMMNS 304
Qy 295 H-FLDGNLVLEGGKVD---ESRREMTRIKDLKQKHPEKDLDQVEMANYALS 351
Db 305 ESEFMDS-AMGFEKEDLDEEBAREVRIILKELKQKHPEKDLDQVEMANYALS 363
Qy 352 AFYRIQATRMATGAGNILKKAEOAKKASMSSEVHTDEPE-DFISKVFPDPSYOCLEN 410
Db 364 AFYRIQATRMATGAGNILKKAEOAKKASMSSEVHTDEPE-DFISKVFPDPSYOCLEN 423
Qy 411 CGAVLLTVARKGDMKTYVDYKTEGDSANAGADYEFTEGTVLKPGETQKEFSGYIID 470
Db 424 CGVAVLVNVRFLGDLTNTVSVYRTEDGTANAGSDYQFTGEGVVFNPGETEKIRIIDID 483
Qy 471 DDIFEEDEHFFVRLSNVRILEEOPREGMPAIFNSJLPRAYLASPCVATVITLDDHAG 530
Db 484 DDIFEEDEHFFVRLSNVRILEEOPREGMPAIFNSJLPRAYLASPCVATVITLDDHAG 540
Qy 531 IFTFECDTIHSVSEIGVMEKVLRTSGARGTVIPRVEGTAKGGEDFEDTGHLEBQ 590
Db 541 IFTFEEPRVMTISSIGMEKVLRTSGARGTVIPRVEGTAKGGEDFEDTGHLEBQ 600
Qy 591 NDETVTIRKIVDEDEYERQENFALGEPKMMENGISDVTDRK-----635
Db 601 NDETVTIRKIVDEDEYERQENFALGEPKMMENGISDVTDRK-----635
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Db 601 NDEIFKSIQIINIDDEYEKKNFLEMGEPOLLE-----MSERKAVLLQIEIGFVKTGR 655  
 Qy 636 -----LPMEEBAKRIAMGKPVLEHPEKLEVIIIES 667  
 Db 656 DYKRYGGRNDPVPATIIISLAEBGDEELSKKEEBERIRIEMGRPIGTENHKELEVIIIES 715  
 Qy 668 YEFRTYDKLIKTKTNLALVGTSHWRDQPMFATVISAAGDEDESEBERLPCFEDYVMH 727  
 Db 716 YEFKNTYDKLIKTKTNLALLIGTNSMRQOFMEATVVS--SGDDDEDECEBEKLPSCFDYVMH 774  
 Qy 728 FLTYFMKVLFAFVCPPTTEYCHGMACEFAVSIILIGMTALIGDLSHFCTTIGLKSQVAVV 787  
 Db 775 FLTYFMKVLFAFVCPPTTEYCHGMACEFAVSIISIGLITLTAFIGDLSHFCTTIGLKSQVAVV 834  
 Qy 788 FVAGTGVPTDFASKAALODVYADASIGNVTSNANVFLGIGLANSVAIYVALOGOE 847  
 Db 835 FVALGTGVPTDFASKAALODVYADAFIGNVTSNANVFLGIGLANSVAIYINSKND 894  
 Qy 848 FHSAGTFLASVYLFTFAFVCISVLLYRRRPHLGELGEGRCCKLATYMLFVSLMLLYI 907  
 Db 895 FRVDPGTLASFVLTFTFAFVAVALVYRRRPEIGELGEGRCGPKIATYTCLEFSLMLMYI 954  
 Qy 908 LFATLEAVCYIKGF 921  
 Db 955 VFSSLEAVCHVKGF 968

## RESULT 13

ID 035157 PRELIMINARY; PRT; 940 AA.  
 AC 035157;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JUN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Sodium-calcium exchanger.  
 GN SLC8A1 OR NCX1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C;  
 RA Shi S., Chang B., Brunner S.R.;  
 RT "Is the Sodium-Calcium Exchanger a Candidate Gene for Mouse Dystrophic  
 RT Cardiac Calciosis?";  
 RL Submitted (May-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF004666; AAB69167.1; -;  
 DR MGD: MGI:107956; SLC8A1.  
 DR InterPro: IPR003644; Calx\_beta.  
 DR InterPro: IPR001623; DnaJ\_N.  
 DR InterPro: IPR004837; NaCa\_Exmemb.  
 DR InterPro: IPR004836; NaCa\_Ex.  
 DR Pfam: PF03160; Calx-beta; 2.  
 DR Pfam: PF01699; NaCa\_Ex; 2.  
 DR PRINTS: PR01259; NACAECHNGR.  
 DR SMART: SM00237; Calx\_beta; 2.  
 DR TIGRFAMs: TIGR00845; caca; 1.  
 DR PROSITE: PSS0076; DNaJ\_2; 1.  
 SQ SEQUENCE 940 AA; 104640 MW; 1E61528CAA62898B CRC64;

Query Match 66.5%; Score 3191.5; DB 11; Length 940;  
 Best Local Similarity 67.2%; Pred. No. 1,1e-224;  
 Matches 631; Conservative 108; Mismatches 139; Indels 61; Gaps 10;

Qy 4 LRLOPLTSAFLHGLVFLVFLNGLRAEAGSGDVPSTGONNESCSSDCKEGVILPIW 63  
 Db 2 LRSLTPNVSMGFRVLAVALSHVDHITADTEAFEGNTECTGCTYCKKGVILPIW 61  
 Qy 64 YPENPSLGDGIARIYIVYFVALIYWFGLVSIADREMASIVINSQEEVVIKKRNGTST 123  
 Db 62 EPDPSFGDGIARIYIVYFVALIYWFGLVSIADREMASIVINSQEEVVIKKRNGTST 121

Qy 124 TTRVNNETVSNLTLMALGSSAPILLSLIEVCGHGIADLGSTIVYSAENMETIIG 183  
 Db 122 TTVRIINMETVSNLTLMALGSSAPILLSLIEVCGHGNFTAGDLPGRISVSAENMETIIG 181  
 Qy 184 ICYVVIDDGEFRKIKHLRVFFITAWMSIFAVIMYMLIAFSPVQVWVGILLTFEPV 243  
 Db 182 LCYVVPDGEFRKIKHLRVFFITAWMSIFAVIMYMLIAFSPVQVWVGILLTFEPV 241  
 Qy 244 CYLLAAVADRRLFLFYKTMHKKYRTDKRGILLIETEGDHPG---IENDGKMNSH---FL 297  
 Db 242 CVFVWAWADRRLFLFYKTYKRYRAGKORGMILIEHGRPRASKTEIENDGKVNSHVNFL 301  
 Qy 298 DGNLVPLEGKVD---ESRREMRILIKDKQKHPEKDLQVEMANYVALSHQOKSRAP 353  
 Db 302 DGNLV-LEVDRODDDEARREMARILIKQKHPEKDLQVEMANYVALSHQOKSRAP 360  
 Qy 354 YRIQATVMKAGAILKHAADQAKKSSSEVITDPE-DIFSKVFDPCSTQCLNCG 412  
 Db 361 YRIQATRLMGAGNILKHAADQAKKSSSEVITDPE-DIFSKVFDPCSTQCLNCG 420  
 Qy 413 AVLLTVYRKGDMSKTYVYKTEDEGSANAGADYEFTGTVLKPGEFQEFVSIIDD 472  
 Db 421 TVALLTVYRKGDLSYTVFVDFRTEDGTANAGSDYEFTEGVIRKPGETOKEIRGIIDD 480  
 Qy 473 IFEDDEHFVRLSNVRIEEOPEEGMPAIFNSLPLRAVLASPCVATVTLDDDHAGIF 532  
 Db 481 IFEDDENFVLHLSNVRRSDVSDGI---LESNASSIACLSPTSTATITIFDNDHTGIF 537  
 Qy 533 TFECDTTHVSESIGVMKVLRTSGARGYIVPPRYTEGAKGGEFEDTGYELEKND 592  
 Db 538 TFECPVTHVSESIGIMEKVLRTSGARGVNIIPKTIETGARGGEFEDTGYEPERND 597  
 Qy 593 EYVTVIRVK-IVDEEYEROENFIALGEPKMMRG----- 627  
 Db 598 EYVTVIRVKIIVDEEYERKNT-PIETGEPRVYMSKKALLNLNLOGFTLTKEMNGOP 656  
 Qy 628 -----ISDVTDRK--LTMEEBAKRIAMGKPVLEHPEKLEVIIIES 667  
 Db 657 IFRKHARHPIPSTVITISSEYVDKQPLRSKEDQERRIEMGRPIGTENHKELEVIIIES 716  
 Qy 668 YEFRTYDKLIKTKTNLALVGTSHWRDQPMFATVISAAGDEDESEBERLPCFEDYVMH 727  
 Db 717 YEFKNTYDKLIKTKTNLALVGTSHWRDQPMFATVISAAGDEDESEBERLPCFEDYVMH 776  
 Qy 728 FLTYFMKVLFAFVCPPTTEYCHGMACEFAVSIILIGMTALIGDLSHFCTTIGLKSQVAVV 787  
 Db 777 FLTYFMKVLFAFVCPPTTEYCHGMACEFAVSIILIGMTALIGDLSHFCTTIGLKSQVAVV 836  
 Qy 788 FVAGTGVPTDFASKAALODVYADASIGNVTSNANVFLGIGLANSVAIYVALOGOE 847  
 Db 837 FVALGTGVPTDFASKAALODVYADASIGNVTSNANVFLGIGLANSVAIYCHANGEO 896  
 Qy 848 FHSAGTFLASVYLFTFAFVCISVLLYRRRPHLGELG 886  
 Db 897 FKVSPGTLASFVLTFTFAFVAVALLYRRRPEIGALFG 935

## RESULT 14

ID 09EP08 PRELIMINARY; PRT; 595 AA.  
 AC 09EP08;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Sodium-calcium exchanger 3 (Fragment).  
 GN SLC8A3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sokolow S., Herchuelz A., Schurmans S.;

"Mus musculus mRNA for sodium-calcium exchanger 3 (NCX3), partial  
sequence."  
RT Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
RL EMBL: AF221404; AAC42826.2; -  
DR MGD; MGI:107976; SIC8a3.  
DR InterPro: IPR003644; Calx\_beta.  
DR InterPro: IPR004837; NaCa\_Extremb.  
DR InterPro: IPR004836; NaCa\_Ext.  
DR Pfam: PF01699; Calx\_beta; 2.  
DR Pfam: PF01699; NaCa\_Ext; 1.  
DR SMART: SM00237; Calx\_beta; 2.  
DR TIGRFAMs: TIGR00845; caca; 1.  
FT NON\_TER 595  
SQ SEQUENCE 595 AA; 66200 MW; 8EF81CBCEDEB7854 CRC64;

Query Match 62.8%; Score 3012; DB 11; Length 595;  
Best Local Similarity 97.5%; Pred. No. 7,66-212;  
Matches 580; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

1 MAMRLRLPGLTSAFLHGLVTLVFLNGLRAEAGSGDVPSTGONNESCSSGSDCKEGVIL 60  
1 MAMRLRLPGLTSAFLHGLVTLVFLNGLRAEAGSGDVPSTGONNESCSSGSDCKEGVIL 60  
61 PIWYRPNLSGDKIARVIVYEVVALIYMFGLVSIADREMASIEVTSOEREYTIKKPGE 120  
61 PIWYRPNLSGDKIARVIVYEVVALIYMFGLVSIADREMASIEVTSOEREYTIKKPGE 120  
121 TSTTIRWNETVSNLTALMALGSSAPEILLSEVCGHGFAGDLGPSTIVGSAFNMFI 180  
121 TSTTIRWNETVSNLTALMALGSSAPEILLSEVCGHGFAGDLGPSTIVGSAFNMFI 180  
181 ITGICVYIPDGETRKIKHLVFEFTAMSTFAVYTWLMTLAVSPGVQWEGLLTFE 240  
181 ITGICVYIPDGETRKIKHLVFEFTAMSTFAVYTWLMTLAVSPGVQWEGLLTFE 240  
241 FPPVCVLLAMVADKRLLEFYKMHKKYRTDKNKGIIETEGDHPKGIEMDGKMMNSHFLDGN 300  
241 FPPVCVLLAMVADKRLLEFYKMHKKYRTDKNKGIIETEGDHPKGIEMDGKMMNSHFLDGN 300  
301 LVPLEGGKVDSESRREMRILKDLKOKHPEKDLQLEMANVYALSHOOKSRAFYRIQATR 360  
301 LVPLEGGKVDSESRREMRILKDLKOKHPEKDLQLEMANVYALSHOOKSRAFYRIQATR 360  
361 MMTGAGNLTAKKHAEOAKSSMSVHTDEPEDFSKVPFPCSYQCLENGAVLLTVVR 420  
361 MMTGAGNLTAKKHAEOAKSSMSVHTDEPEDFSKVPFPCSYQCLENGAVLLTVVR 420  
421 KGDMSKTMVYDYKTEDEGSANAGADYEFTEGTVVLPGETOKEFESVGIIDDI FEDEDEHF 480  
421 KGDMSKTMVYDYKTEDEGSANAGADYEFTEGTVVLPGETOKEFESVGIIDDI FEDEDEHF 480  
481 FVRLSNVRIEEOPBEGMPAIFNSLPLPRAVLASPCVAVTITLDDHAGITFECDTIH 540  
481 FVRLSNVRIEEOPBEGMPAIFNSLPLPRAVLASPCVAVTITLDDHAGITFECDTIH 540  
541 VSESGVVEVVLRTSGRGTVIVPFRVETGAKGGGEDEFTVGELEFKNDETY 595  
541 VSESGVVEVVLRTSGRGTVIVPFRVETGAKGGGEDEFTVGELEFKNDETY 595

RESULT 15  
002196 PRELIMINARY; PRT; 892 AA.  
AC 002196;  
DT 01-JUL-1997 (TREMBLrel. 04, Created)  
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE NaCa exchanger.  
GN NCX-SOL.  
OS Loigo opalescens (California market squid).  
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Teuthoidea;  
OC Myopoda; Loliginidae; Loligo.  
OX NCBI\_Taxid=31211;

RP {1}  
SEQUENCE FROM N.A.  
RA He Z., Phillips K.D.;  
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U93214; AAB52920.1; -  
DR InterPro: IPR003644; Calx\_beta.  
DR InterPro: IPR004837; NaCa\_Extremb.  
DR InterPro: IPR004836; NaCa\_Ext.  
DR Pfam: PF01699; Calx\_beta; 2.  
DR Pfam: PF01699; NaCa\_Ext; 2.  
DR PRINTS: PRO1259; NACAEXCHGR.  
DR SMART: SM00237; Calx\_beta; 2.  
DR TIGRFAMs: TIGR00845; caca; 1.  
SQ SEQUENCE 892 AA; 98517 MW; ED140163F2473700 CRC64;

Query Match 52.8%; Score 2533; DB 5; Length 892;  
Best Local Similarity 57.1%; Pred. No. 1,66-176;  
Matches 516; Conservative 145; Mismatches 213; Indels 30; Gaps 14;

23 LFLNGLRAEAGSGDVPSTGONNESCSSSD-CKEGVILPIWYR-ENPSLDGKIRATVY 80  
14 LFLGLFFDFAHASE-----DSNDCTTEAETCRNGLVPRNPNGLNSVGDKLARATVY 68  
81 FVALIYMFGLVSIADREMASIEVTSOEREYTIKKPGETSTTIRWNETVSNLTALMA 140  
69 FVLMRYTLFGLVSIADREMASIEVTSKEDVYKPPGCTTVVNRITNETVSNLTALMA 128  
141 LGSSAPEILLSEVCGHGFAGDLGPSTIVGSAFNMFIITGICVYIPDGETRKIKHL 200  
129 LGSSAPEILLSEVYVGQKFEAGQLGPSTIVGSAFNMFIITGICVYIPDGETRKIKHL 188  
201 RVFFTTAMSTFAVYTWLMTLAVSPGVQWEGLLTFEPFVCVLLAMVADKRLLEFYK 260  
189 GVFFTTAMSTFAVYTWLMTLAVSPGVQWEGLLTFEPFVCVLLAMVADKRLLEFYK 247  
261 MHKKYRTDKNKGIIETEGDHPKGIEMDGKMMNSHFLDGNLVPLEGGKVDSESRREMRIL 320  
248 LSKTKRAKQKGVYIQCGODAEAGE--GKSDGALKEGG--DDEVREFEQDKRKETIEL 304  
321 KDLKOKHPEKDLQLEMANVYALSHOOKSRAFYRIQATRMWTGAGNLTAKKHAEOAKKA 380  
305 REMRKKNFTLDMKTLDEDAEAEAVNRGPRKRAFYRIQATRKTLTGSGNIIKK--AKAOGVA 363  
361 SSMSEVHTDEPEDFSKVPFPCSYQCLENGAVLLTVVRKGDMSKTMVYDYKTEDEGS 440  
364 QPI--VIDQRPDELTRSFDPGHATVMEVNGTFYGTAREGDLTKLTYDYKTEDEGTA 421  
441 NAGADYEFTEGTVVLPGETOKEFESVGIIDDI FEDEDEHFVRLSNVRIEEOP--EEGM 498  
422 NAGSYVYABGLVYRPMETHKQFPISTIIDDIFEEDEHFYRLSNLKVGDGNGLFEESQ 481  
499 PPAIFNSLPLPRAVLASPCVAVTITLDDHAGITFECDTIHVSISGVEVYKRLTSGA 558  
482 AEA-----KAQLANFLATVMTLDDHDPFIQIDKEMSVTSSEVEVRIITSGA 533  
559 RGTIVVPRVYBGTAAGGGEDEFTVGELEFKNDETIVTIRKIVYDEEYKEQENFFAL 618  
534 RGVAVVPRVHSDGVAT--GKQDVELVDKQVITFENDETEFRLARVAVDDEYENEFFTWL 592  
619 GEPKMERGISDVTDRKLTMEEEAKRIAEMKPVLEGHPKLEVIIESEYKFTVDRKL 678  
593 DEPIYLVKKPTGSSG---SVEDDDPVLAELGKPRGRGNIKITVHIISTEKSAAVDKLL 649  
679 KKTNLALVGTSHWDQFMEALITVSAAGDEDESEGERLPSCFDYVNHFTLVFKVLPA 738  
650 KKANSLVYAGTSVWREQTEALITVNAEGDDDESEEEKLSCMDYIMHFCVCLFKVLLA 709  
739 CVPREYCHGNACFAVSLIIGMLTAIGDLASHGCGITGLKDSYTAAYVFAFGSVYDT 798  
710 FVPPPDVYWGACFTVYSIILGLVLAFTGDLATYFGCTIGLKDAYTAASFAVALGTSVDT 769  
799 FASKAAALQDVADASINVTGNSAVNVLGIGLMSVAATYMALOGEPIHVSAGTLAFS 858

Db 770 FASKVAINDKYADSSIGNVTGSGNAVNVFLGICIANSAIAIYHANGTVFRVDPGTLAFS 829  
OY 859 VLEFTEAFVCIISVLLYRRPHL-GGELGGPRCKLATWLFVSLMLTYLFATLEACY 917  
Db 830 VTIFCVFA-VCTIVLLVCRHHLVGBELGSPRCKYITSGILGFWVSYLLTGLMSYCH 888  
OY 918 IKGF 921  
Db 889 IPGF 892

Search completed: November 30, 2002, 12:30:55  
Job time : 62.9734 secs